

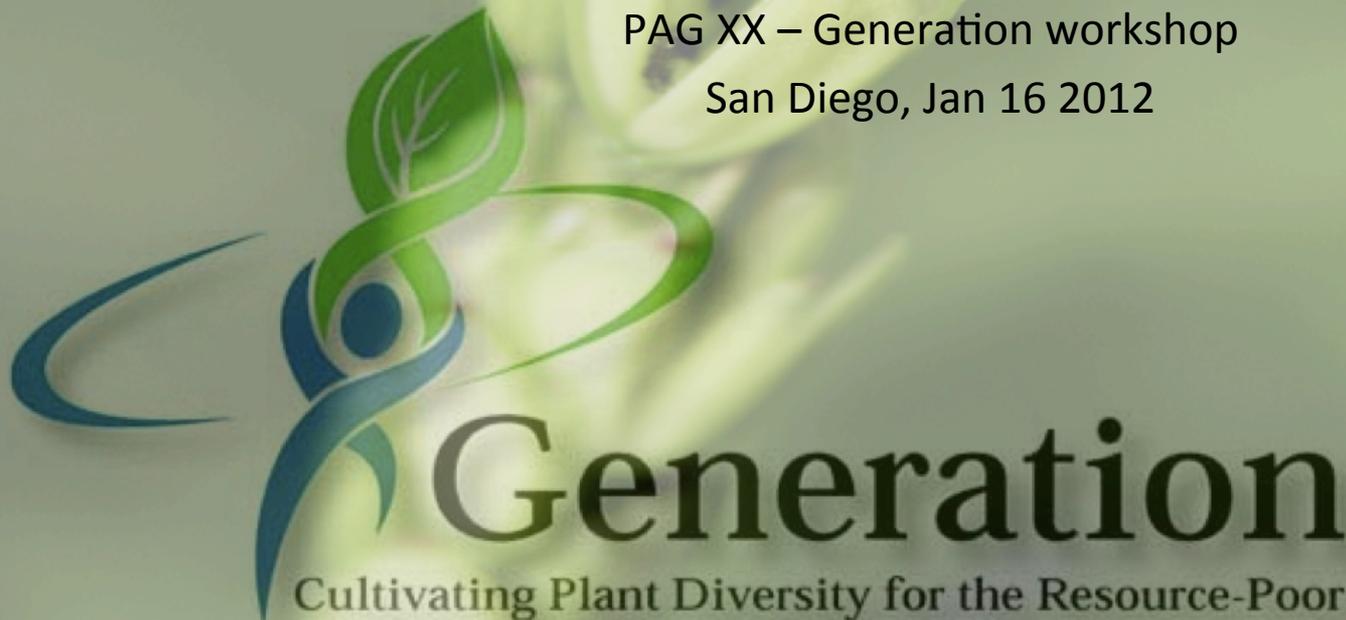
# Genetics of the reproductive barrier between the two cultivated species of rice

Mathias Lorieux

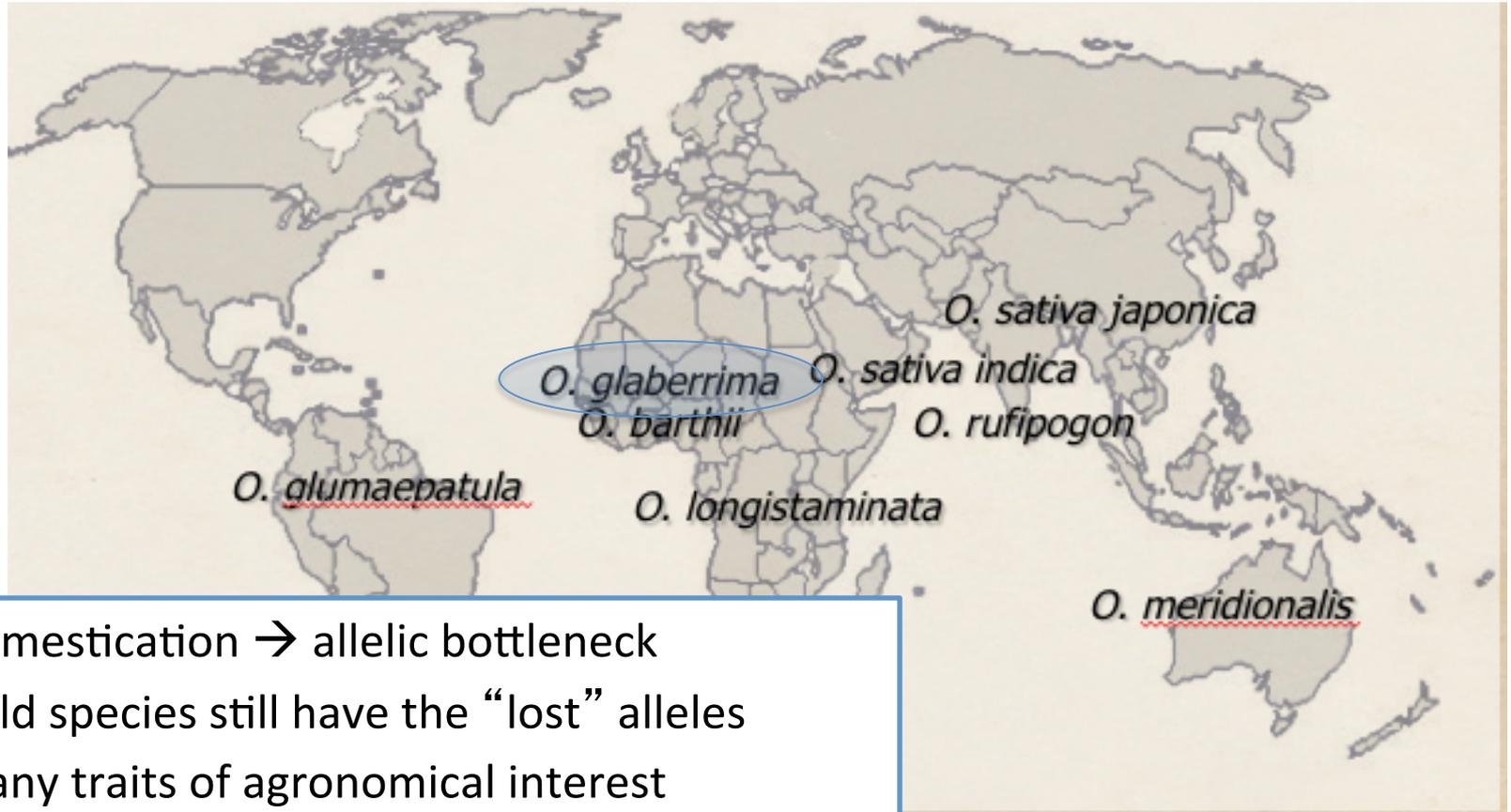
IRD-CIAT Rice Genetics and Genomics Laboratory

PAG XX – Generation workshop

San Diego, Jan 16 2012

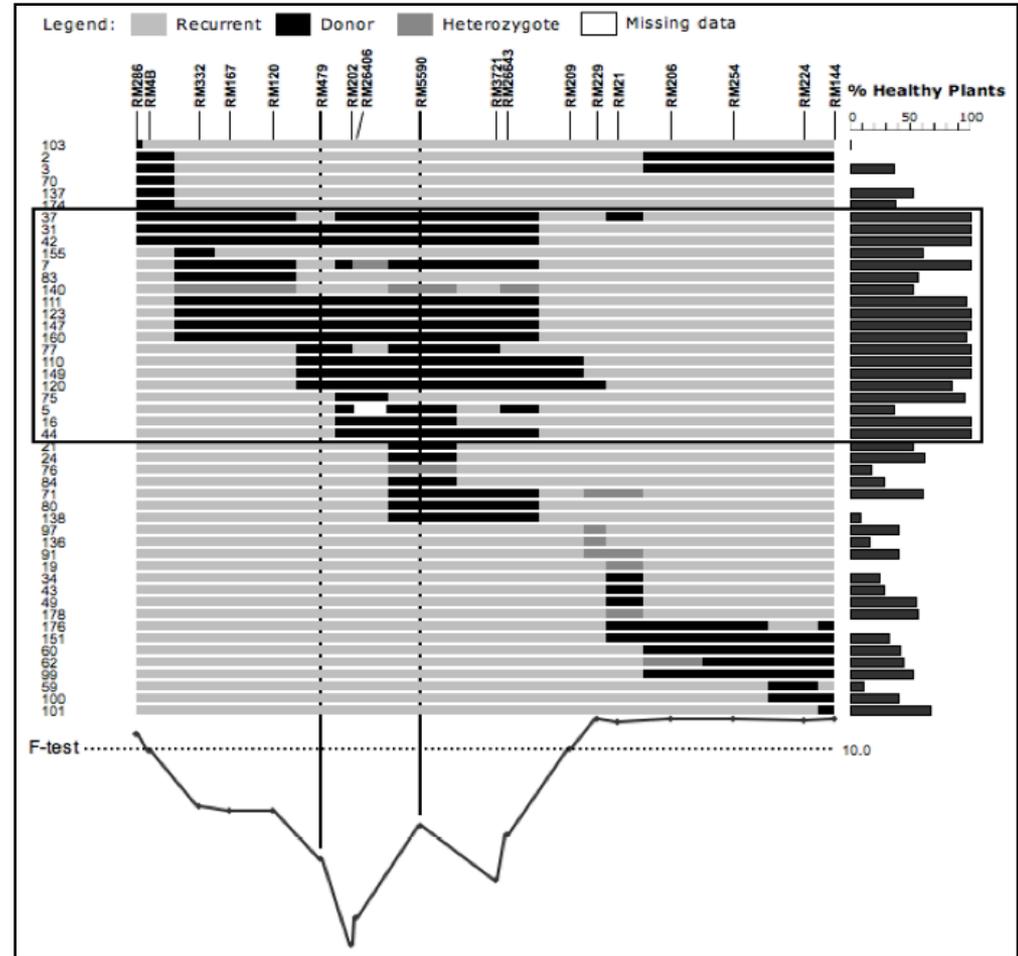
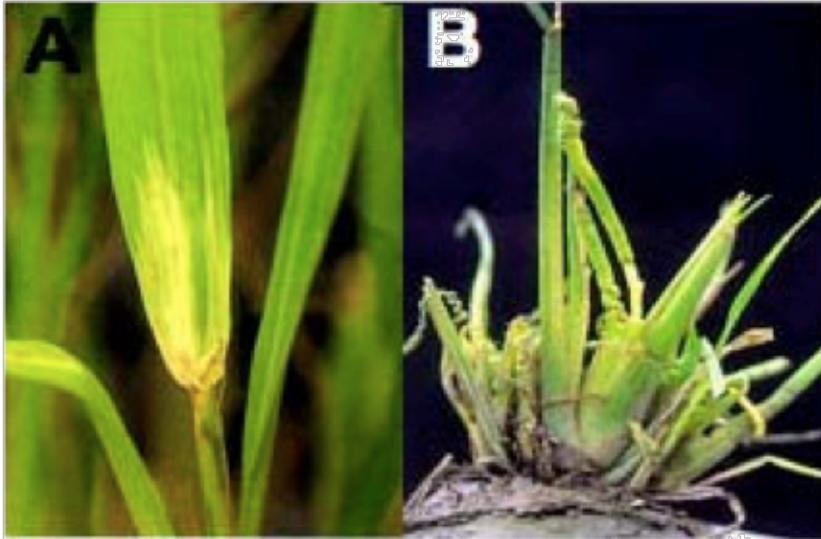


# Using AA genome species of rice to discover genes of importance



- Domestication → allelic bottleneck
- Wild species still have the “lost” alleles
- Many traits of agronomical interest
- Several examples of successful introgression
- *Transgressive* effects

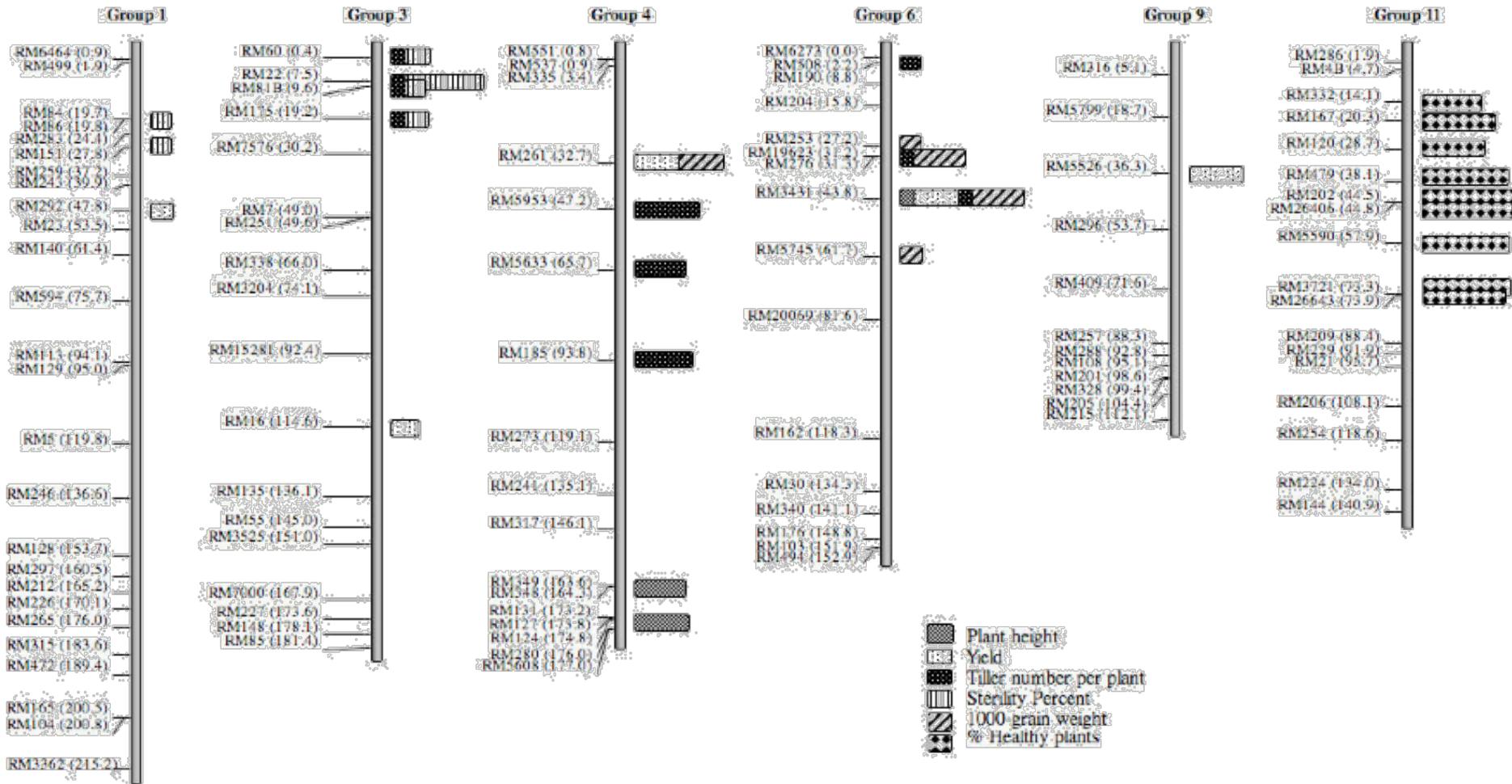
# Mapping of a major resistance gene to *Rice stripe necrosis virus* from *O. glaberrima*



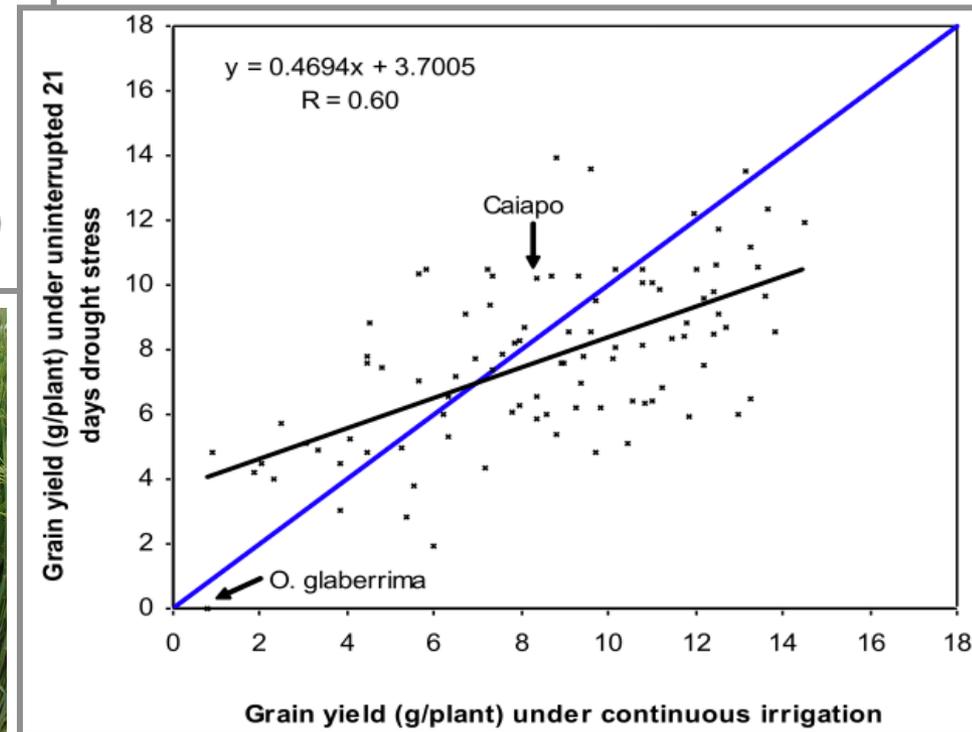
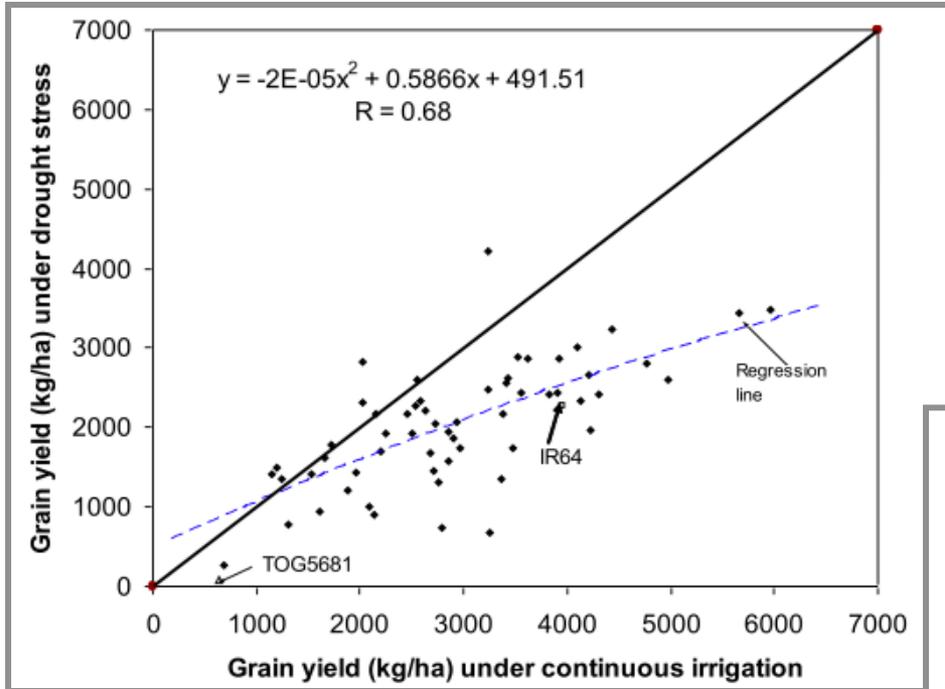
Caiapo x MG12

Gutierrez et al, BMC Plant Biol. 2010

# Yield components QTLs



# Performance of *O. sativa* x *O. glaberrima* ILs under drought



B. Manneh  
(AfricaRice)

# *O. sativa* x *O. glaberrima* reproductive barrier

- One of the strongest post-zygotic reproductive barrier in *Oryza* species
- F1 hybrids:
  - Totally male sterile
  - Partially female sterile
  - $S_1$  is the main factor (Sano 1990)
- $S_1$  limits the use of *O. glaberrima* in breeding
- There are natural hybrids



# Sterility genes cause SD

- Because they favor specific alleles, sterility genes cause **segregation distortion** in progeny
- They are Transmission Ratio Distorters = TRDs
- Many examples in animals and plants
- In rice, TRDs are frequently found in indica x japonica and interspecific crosses
- In *O. sativa* x *O. glaberrima* crosses,  $S_1$  causes extreme SD, with  $f(S_1^g) = 0.9 - 0.98$

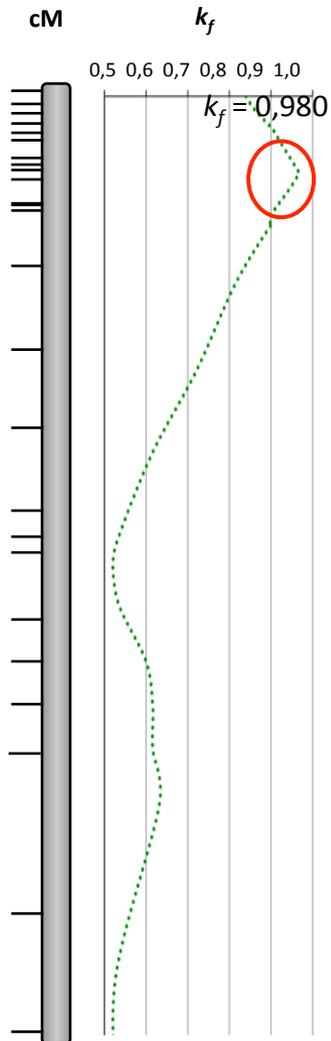
# Mapping TRDs: approaches

- “Classical” mapping strategy
  - Segregation analysis based on marker-phenotype co-analysis (eg pollen fertility)
  - Several (many) backcrosses required
  - Time & resource consuming
- Segregation distortion analysis
  - Based on marker segregation only (eg fTRD statistic)
  - No phenotyping required
  - Early generation analysis (BC1)

# fTRD in 4 BC1 *O. sativa* x *O. glaberrima* populations

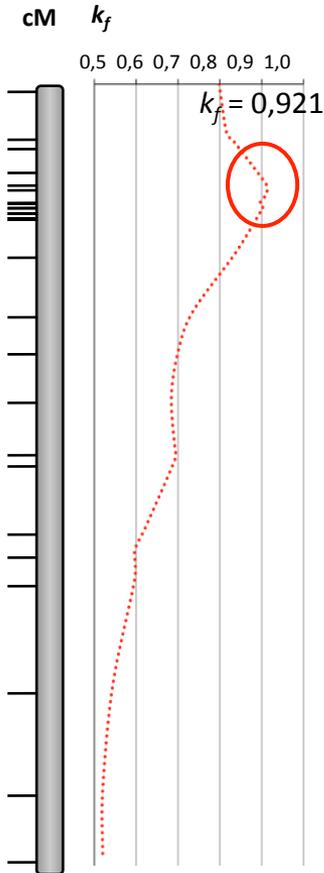
IR64 x TOG5681

n = 459



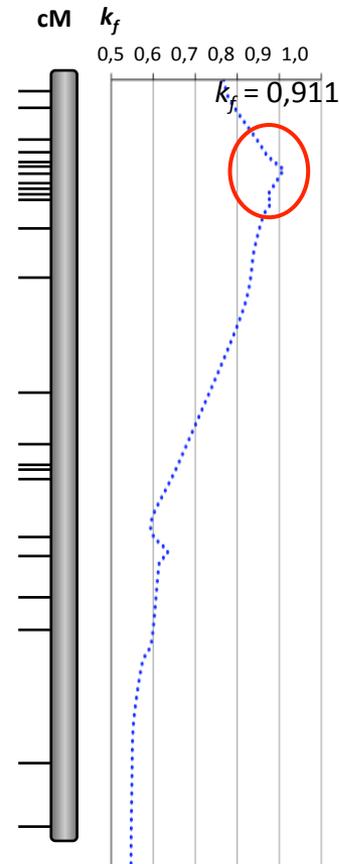
Caiapo x MG12

n = 114



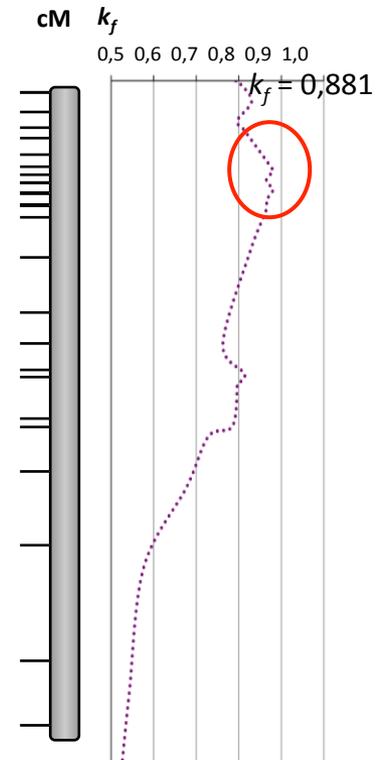
Curinga x CG14

n = 101



Nipponbare x MG12

n = 59

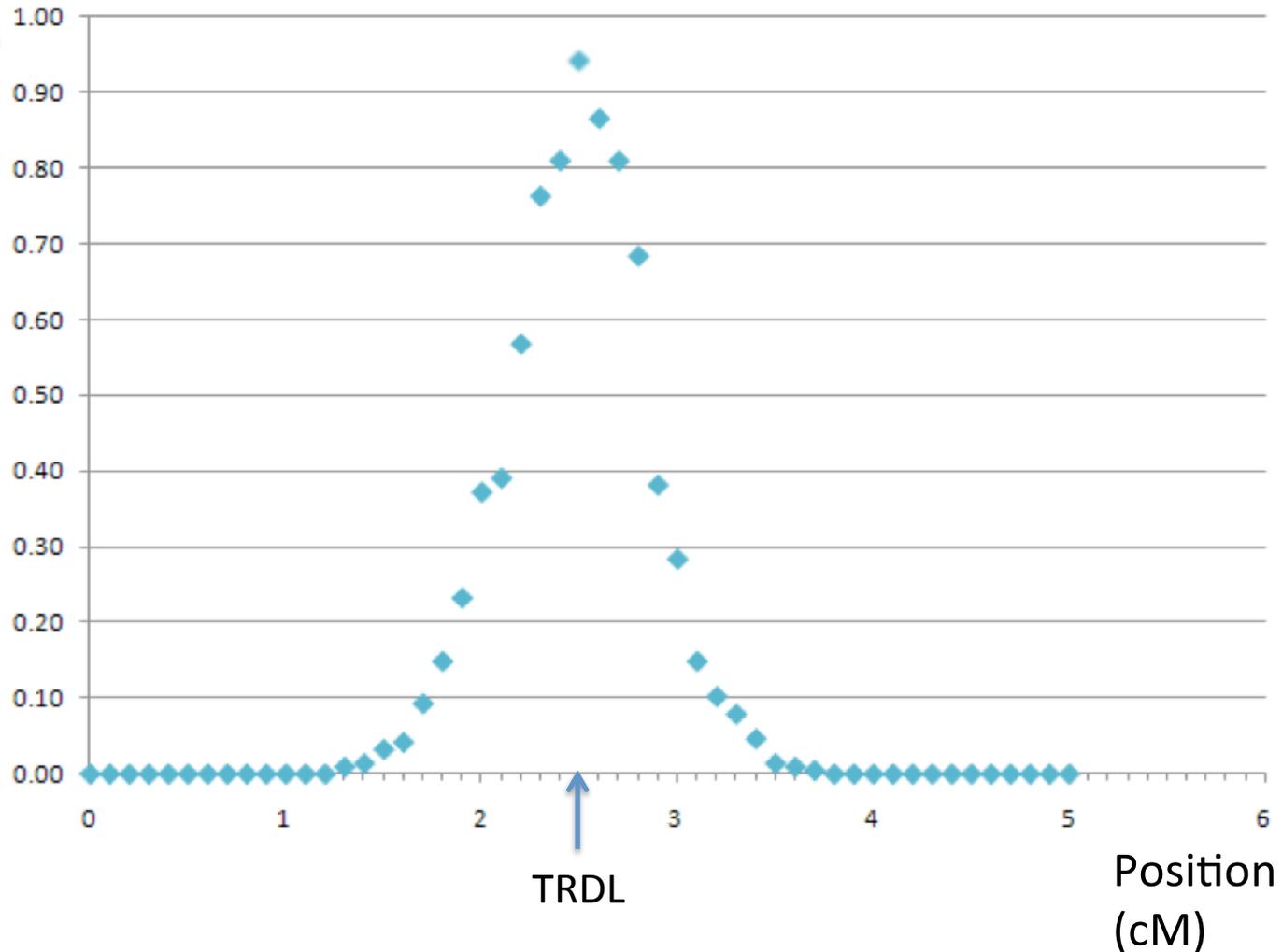


# Mapping TRDs using SD analysis: simulations

% of  $k_{max}$  values  
around the  
TRDL

**Parameters:**

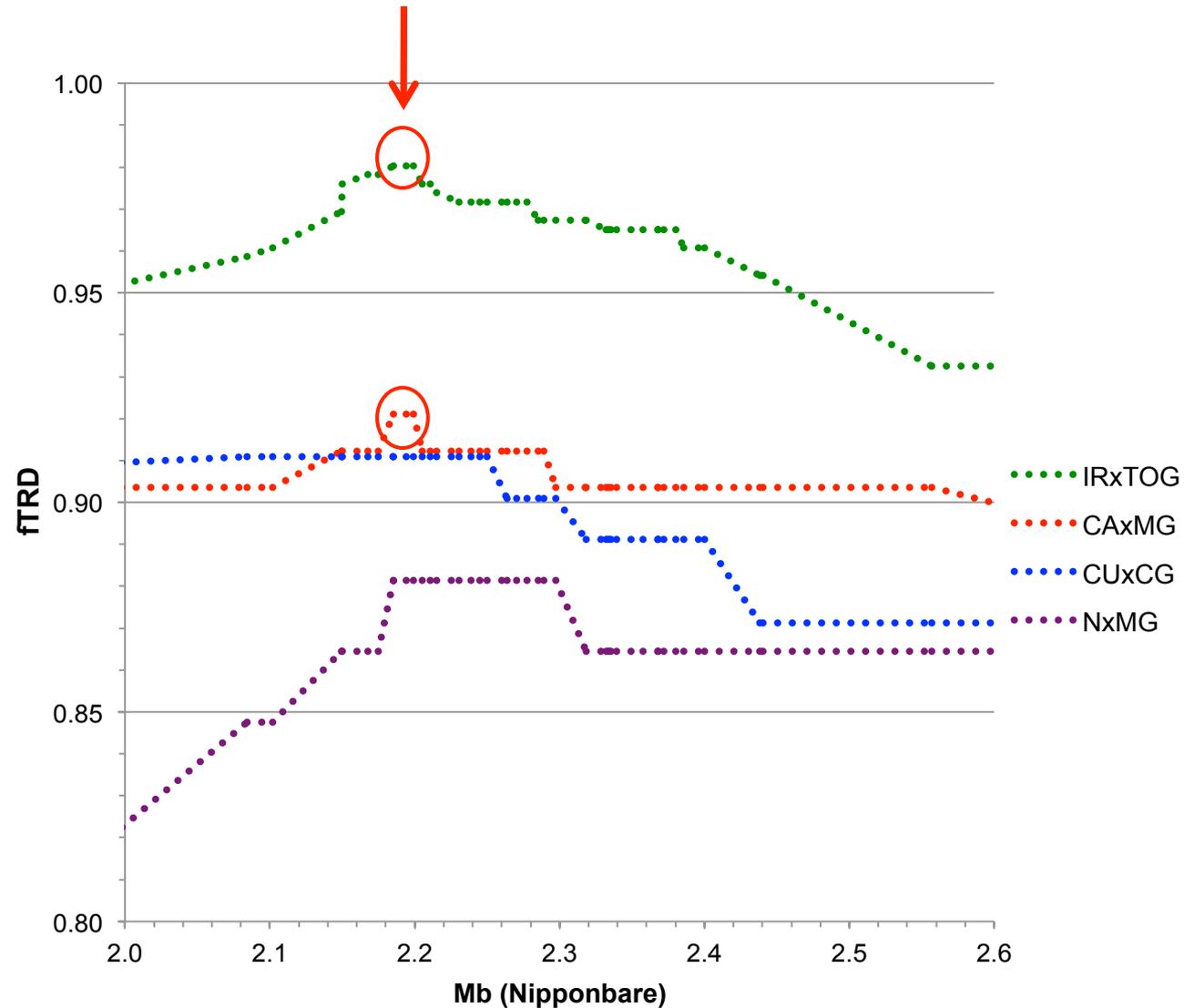
10,000 BC1 pops  
734 indiv each  
5 cM interval  
1 mk / mM  
TDR at 2.5 cM  
 $k = 0.95$



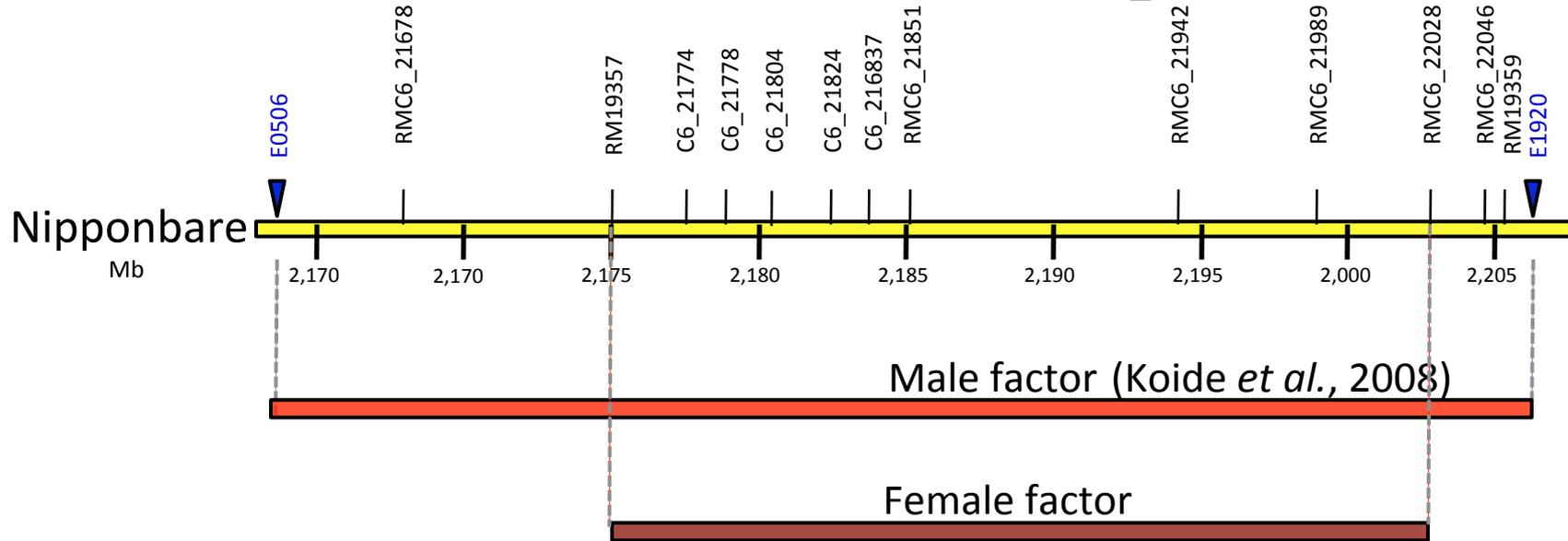
95% of  $k_{max}$  values in a 24 kb interval

# Fine mapping of the $S_1$ locus

- About one marker/gene
- SSRs and RBIPs

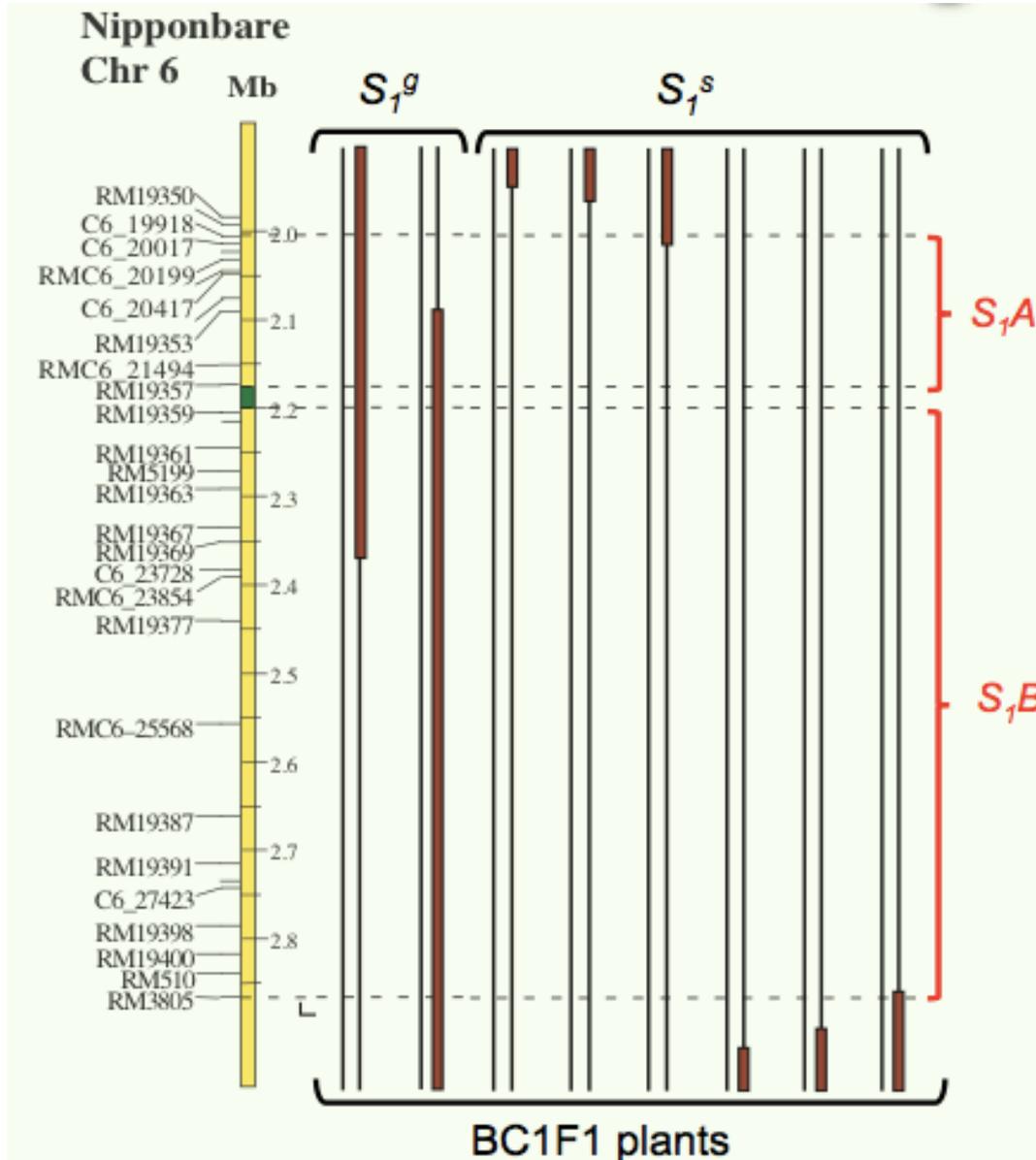


# Fine mapping of the $S_1$ locus



- Female factor in a 27.8 kbp region nested in the male factor region
- Both male and female gamete elimination are probably controlled by the same factor(s)

# $S_1^s$ viable gametes are never recombined around $S_1$



japonica x *O. glaberrima*:  
inherited segment of at least  
7.3 cM in 36 individuals

$$p_0 = (1 - 0.0725)^{36} = 0.066$$

→  $S_1^A$  and  $S_1^B$

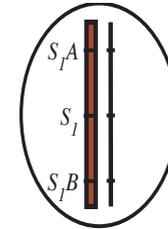
indica x *O. glaberrima*:  
Min = 51.5 cM in 9 individuals

$$p_0 = (1 - 0.387)^9 = 0.012$$

→  $S_1^C$

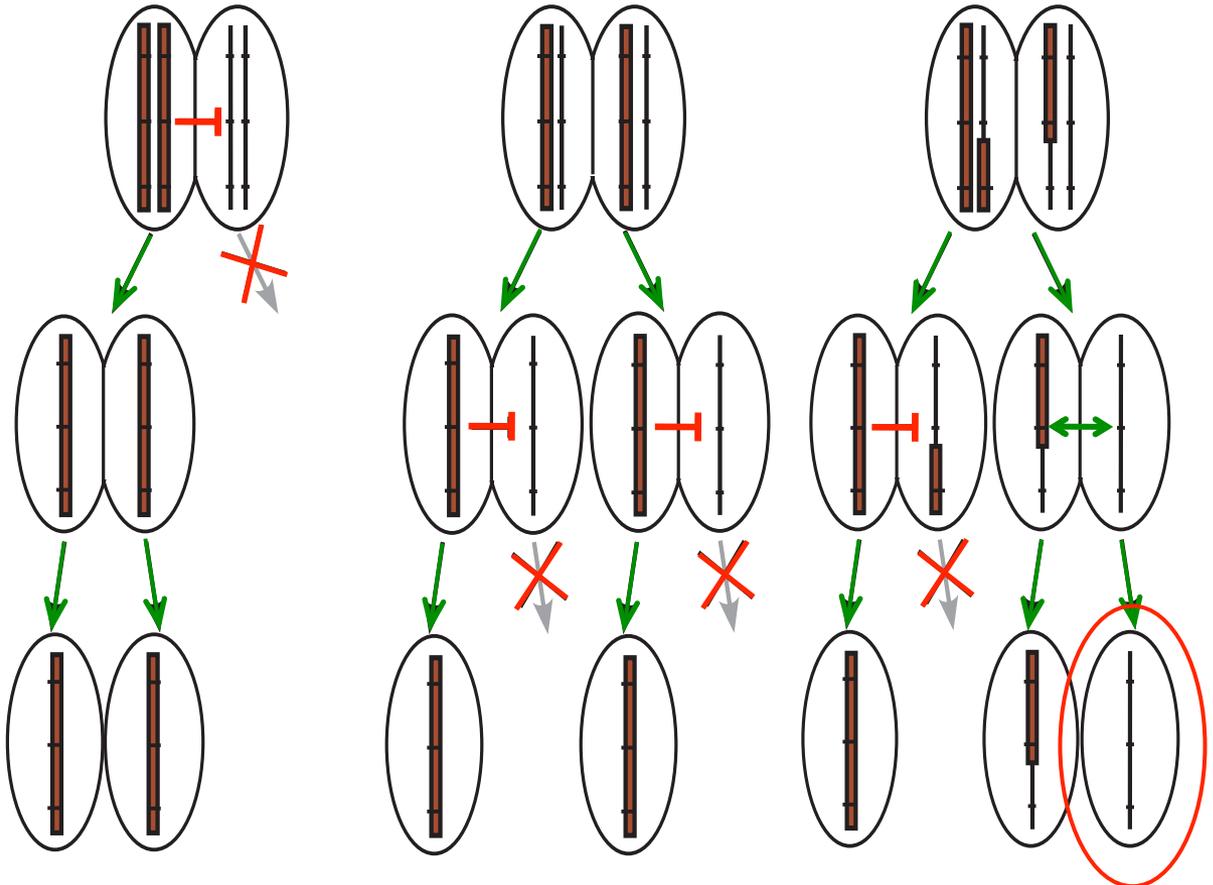
# Genetic model of female gamete elimination

Megasporocyte ( $2n$ )



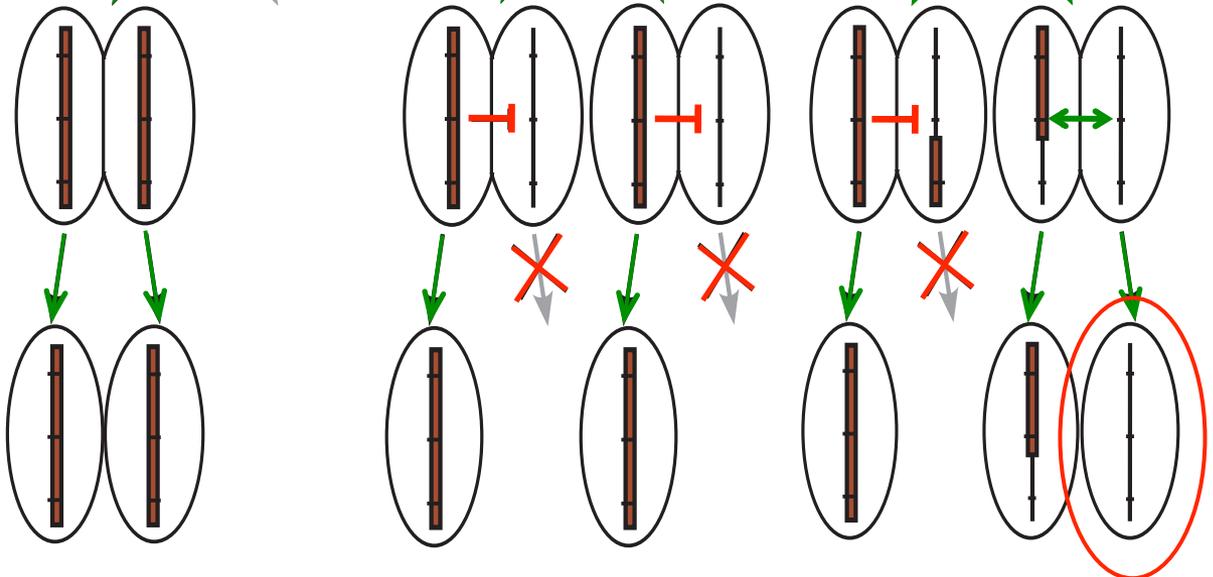
Recombination

First meiotic division  
( $1n - 2c$ )

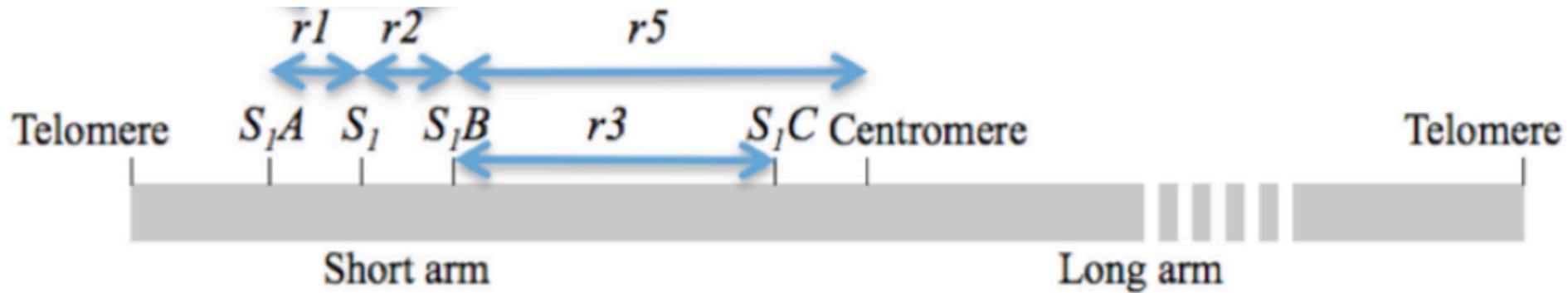
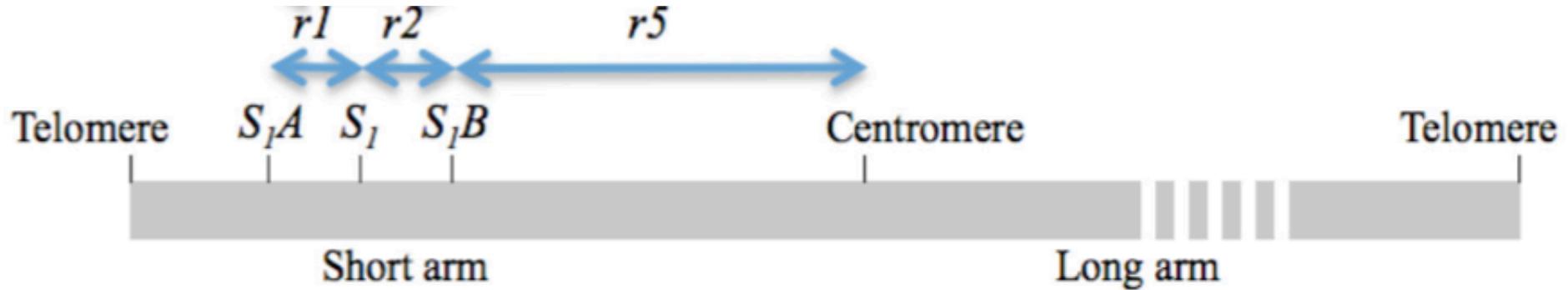


Second meiotic division  
( $1n - 1c$ )

Megaspores



# japonica and indica models



# Genetic model for $S_1$ action

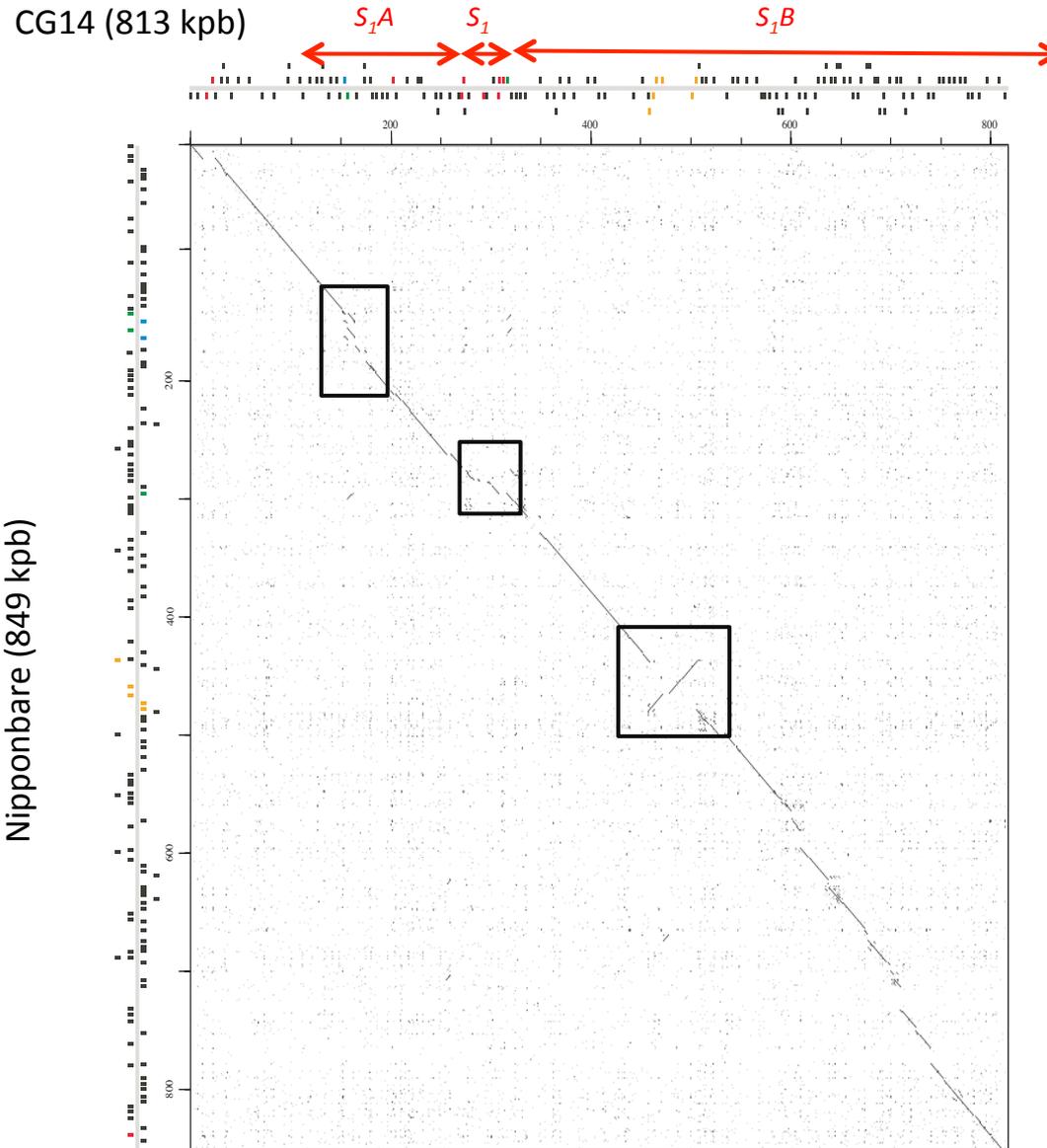
$$f(S_1^s) = \left[ \frac{r_2}{2} + r_5(r_1 - r_2 - 2r_1r_2) \right] / D$$

$$D = (1 - 2r_5) \left( \frac{r_2 + 1}{2} \right) + 2r_5 \left[ \frac{1}{2} + \frac{r_1}{2} - r_1r_2 \right] \text{ (viability of female gamete)}$$

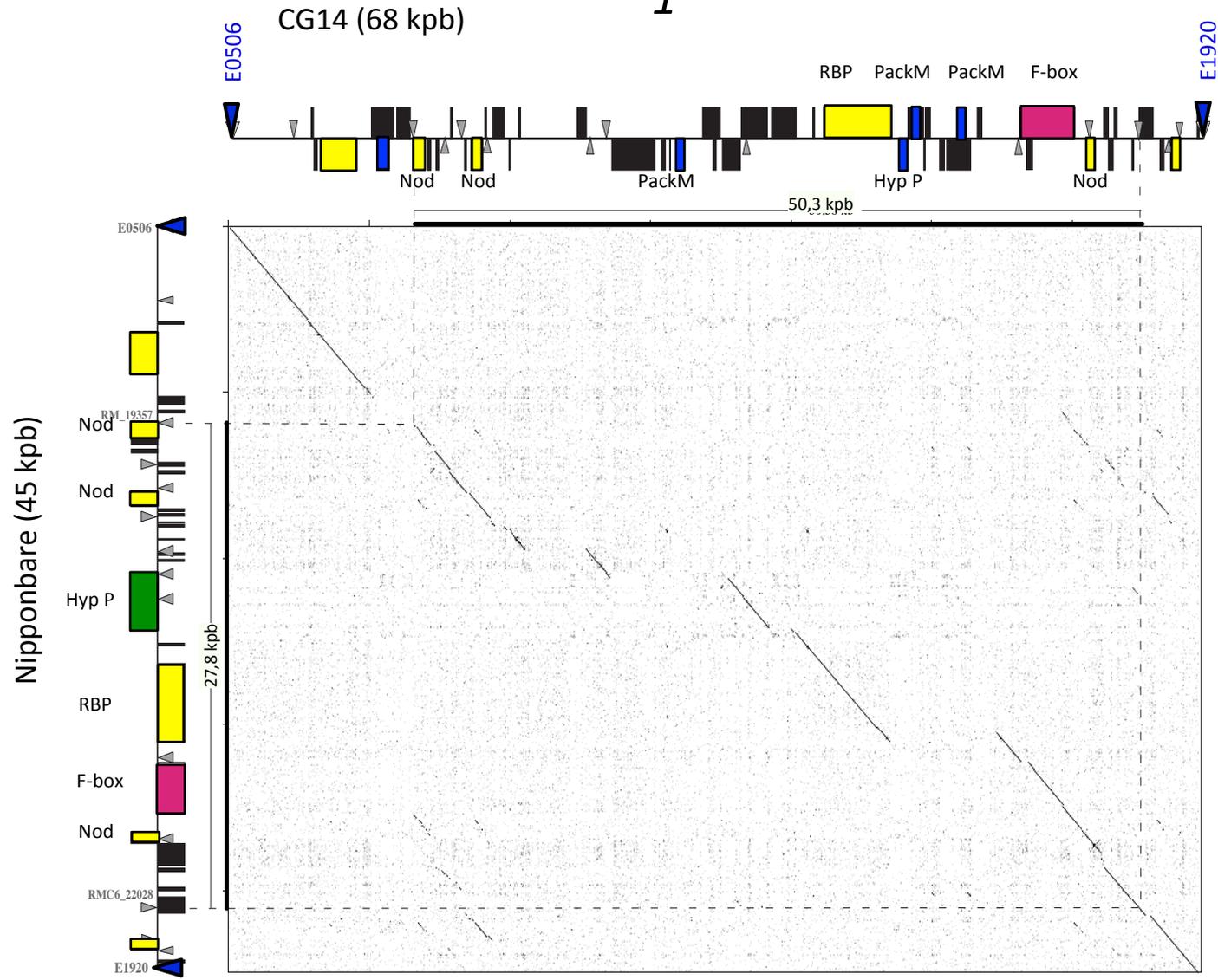
japonica	Observed	Predicted
D	0.51-0.55	0.53
f(S1s)	0.02-0.10	0.04

- Model accurately predicts allelic frequencies & gamete viability
- Maternal allelic transmission depends on recombination around  $S_1$

# *O. sativa* – *O. glaberrima* sequence comparison

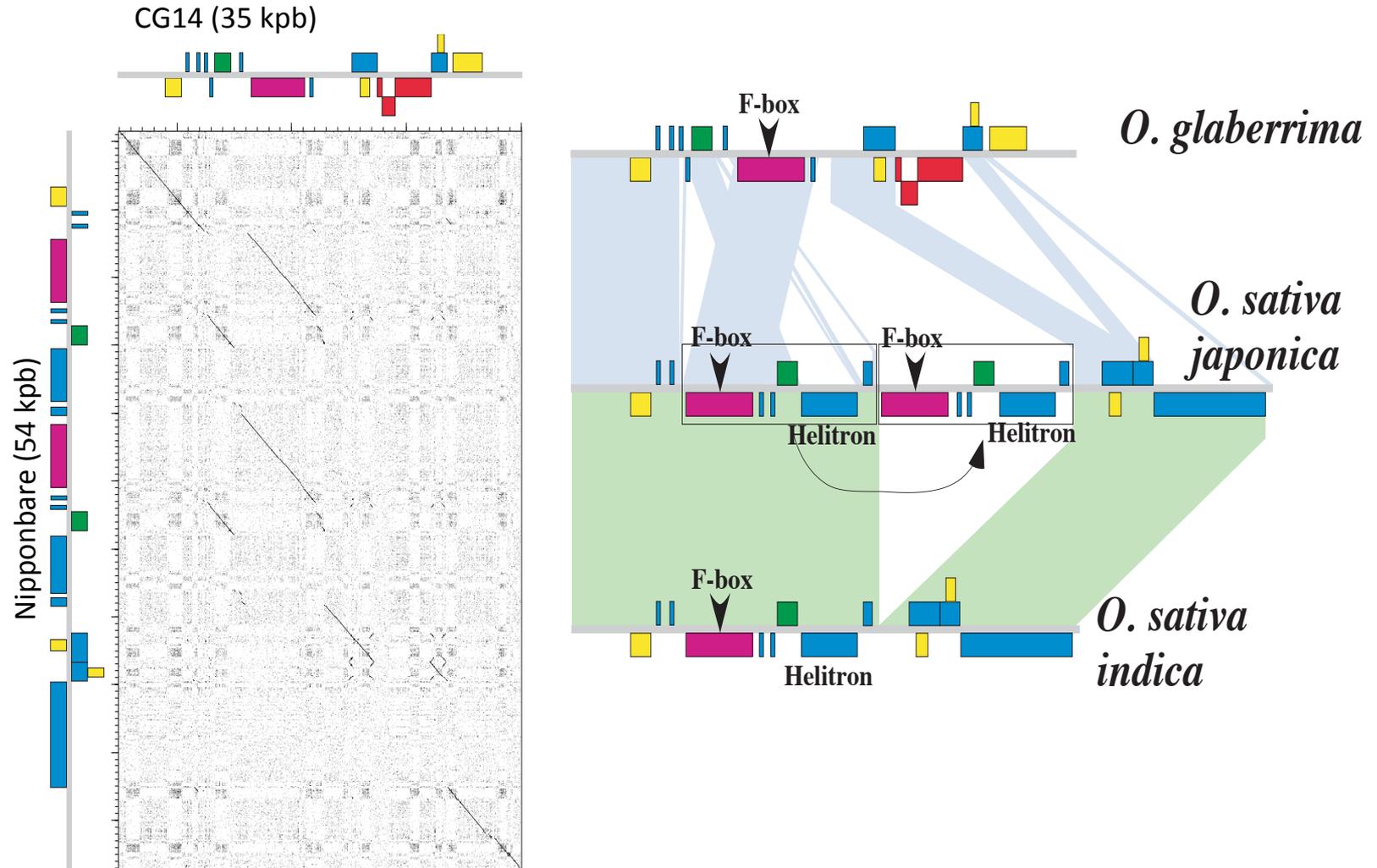


# The $S_1$ locus



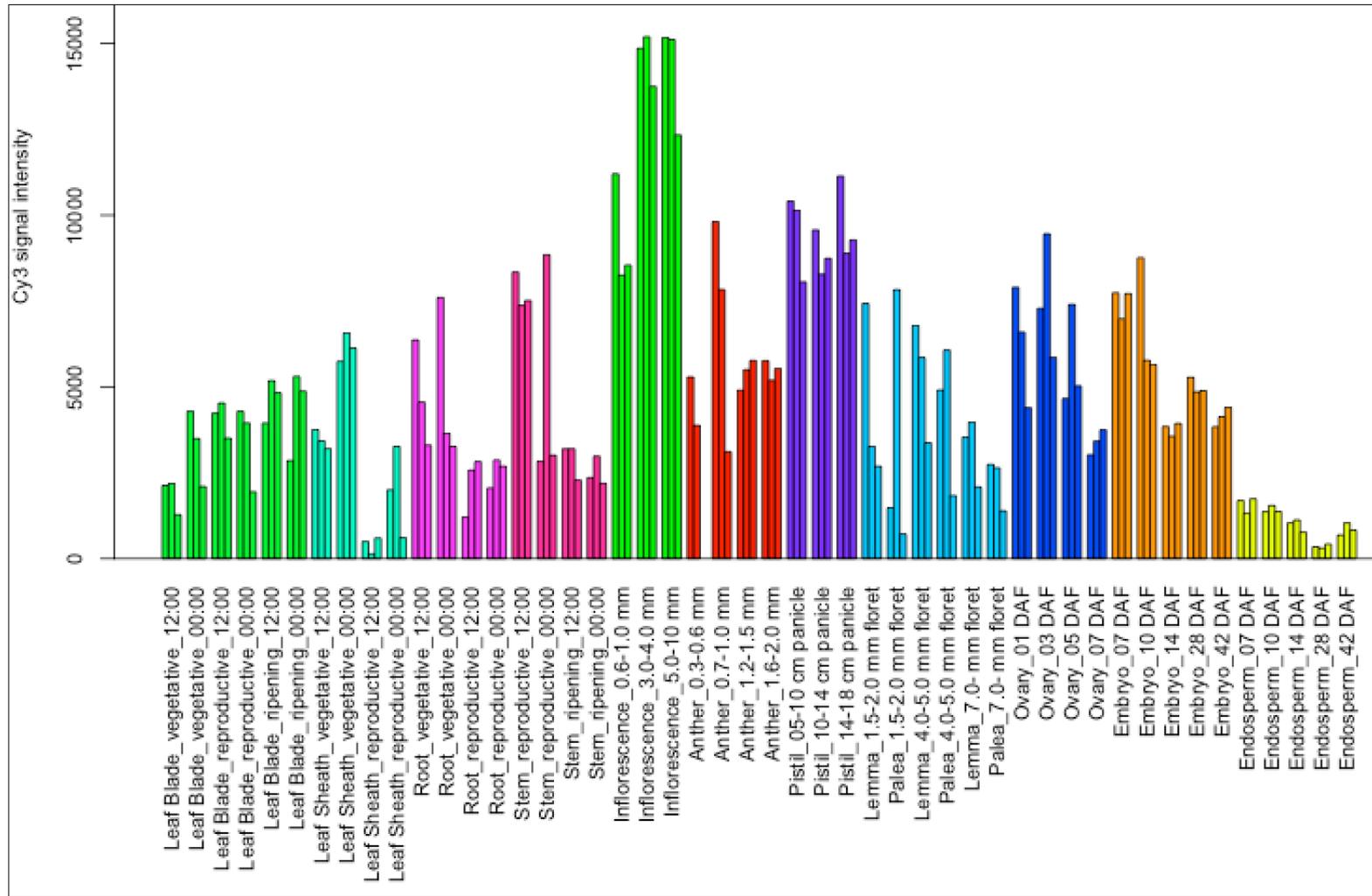
→ Intergenic rearrangements

# The $S_1A$ locus

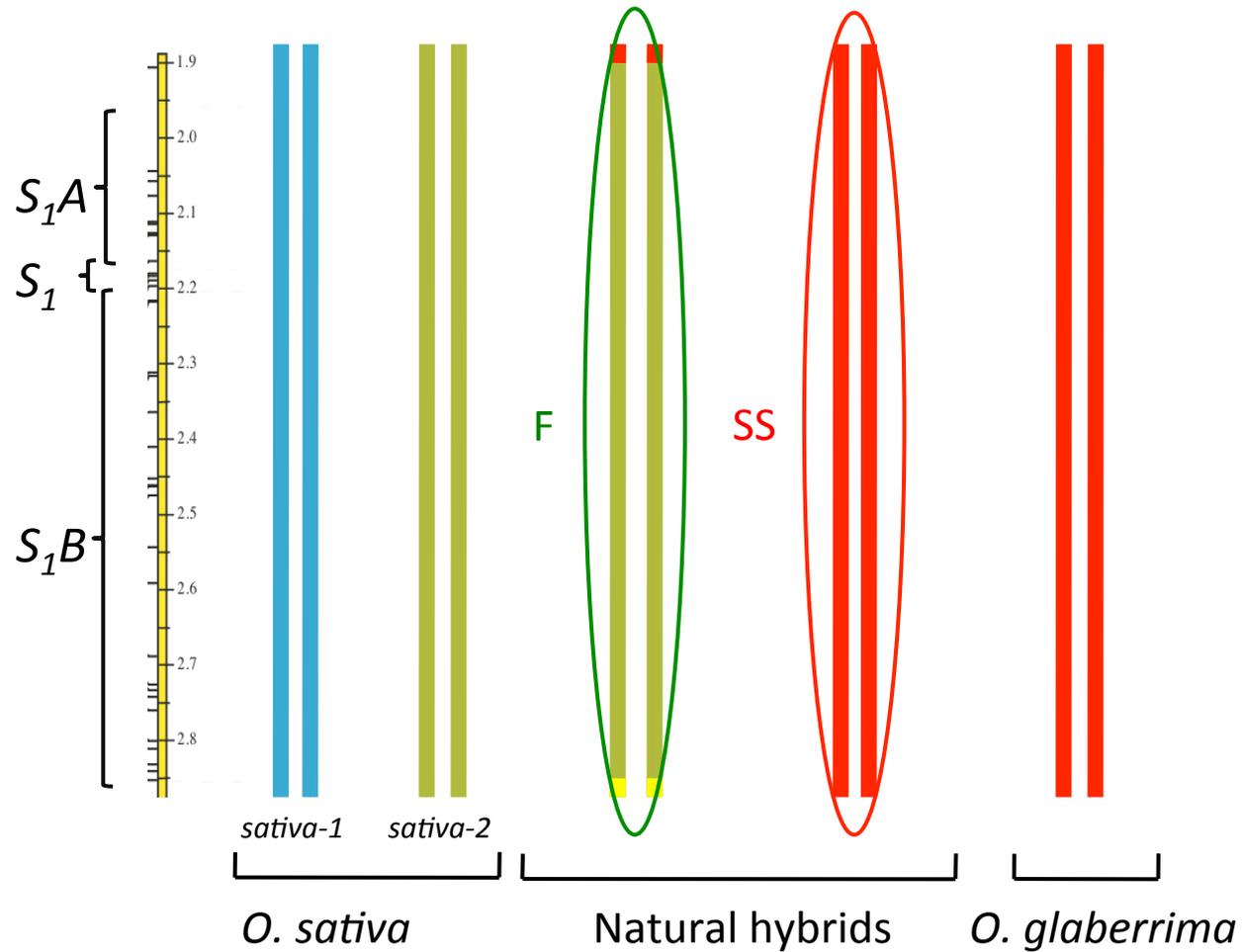


- Important rearrangements
- $F$ -box duplicated between  $S_1$  &  $S_1A$  → BDM model?
- Additional duplication in Nipponbare

# F-Box as candidate for $S_1$ & $S_1A$

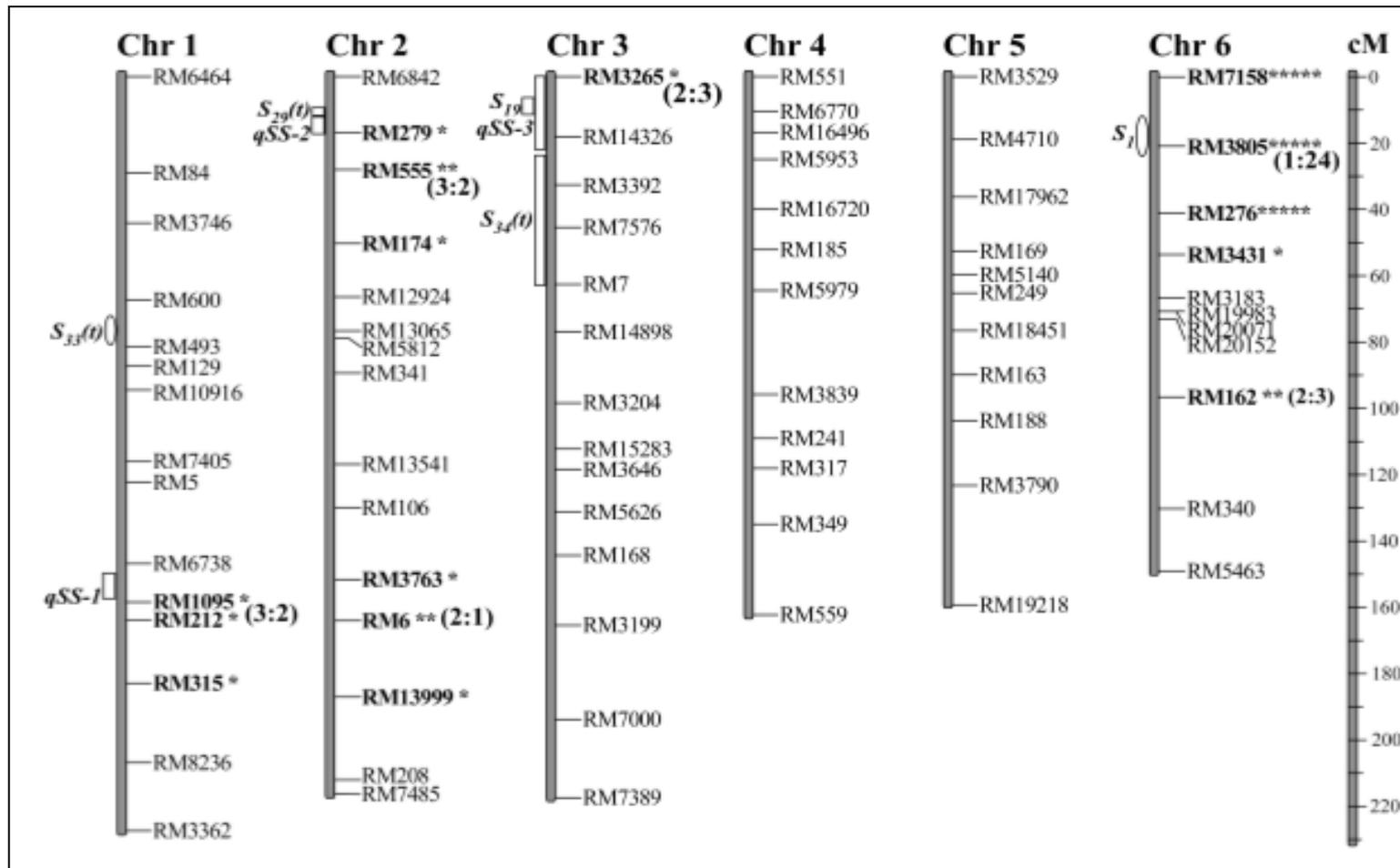


# $S_1$ region haplotypes in natural introgressions



# Other sterility genes

- Either act alone or interact with  $S_1$
- Towards a complete genetic model for the reproductive barrier

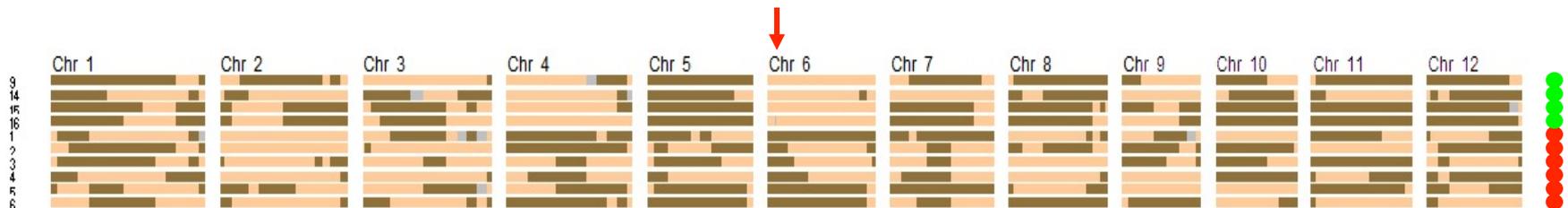


# Generation project: iBridges

The *O. sativa* x *O. glaberrima* sterility barrier hampers full use of interspecific lines in breeding programs

- Although *O. sativa* x *O. glaberrima* introgression lines (like CSSLs) can be fertile, they generally produce partially **sterile hybrids** with *O. sativa*
- Sterility hampers full use of African rice for breeding

→ interspecific bridges



25 glaberrima x 3 sativa

# iBridges outcomes

- 75 pools of BILs, compatible to *O. sativa*
  - 20-25% of *O. glaberrima* genes
- iBridges will facilitate significantly the use of the genetic diversity available in African rice
- *O. sativa* x *O. glaberrima* reproductive barrier
  - Genetic markers around the  $S_1$  sterility gene
  - Allow quick screening for *O. sativa* compatible allele of  $S_1$
  - A map of the *O. sativa* x *O. glaberrima* sterility genes
  - Allow development of even more efficient strategies for future selection of materials
- A technology for developing additional iBridges between *O. sativa* and its other AA-genome (wild) relatives
  - Provide a broad access of the genetic diversity in the AA species complex

# First iBridges

- CIAT, AfricaRice, PhilRice
  - 40% of the BC1F1 lines are fertile vs < 5% without selection

## Next-generation iBridges

- Selection on  $S_1$  + other sterility loci
- Improved crossing scheme
- Also *O. glaberrima* background compatible with *O. sativa*

# Credits & Thanks



## IRD

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## AfricaRice

M. N. Ndjondjop

## PhilRice

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